

Applicant: Rajasekhar Bandaru

Title: 68730 and 69112, Protein Kinase Molecules and Uses
Therefor

Attorney/Agent: Jill Uhl

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Sheet 1 of 8 Sheets

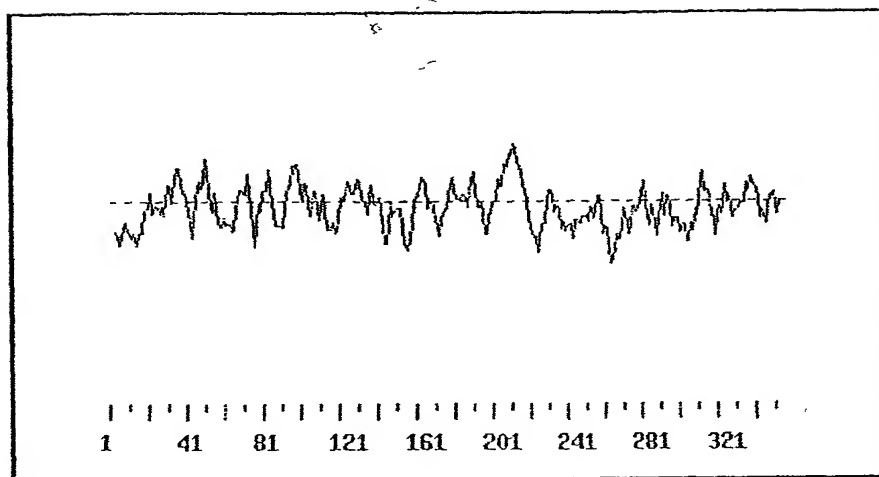


FIGURE 1

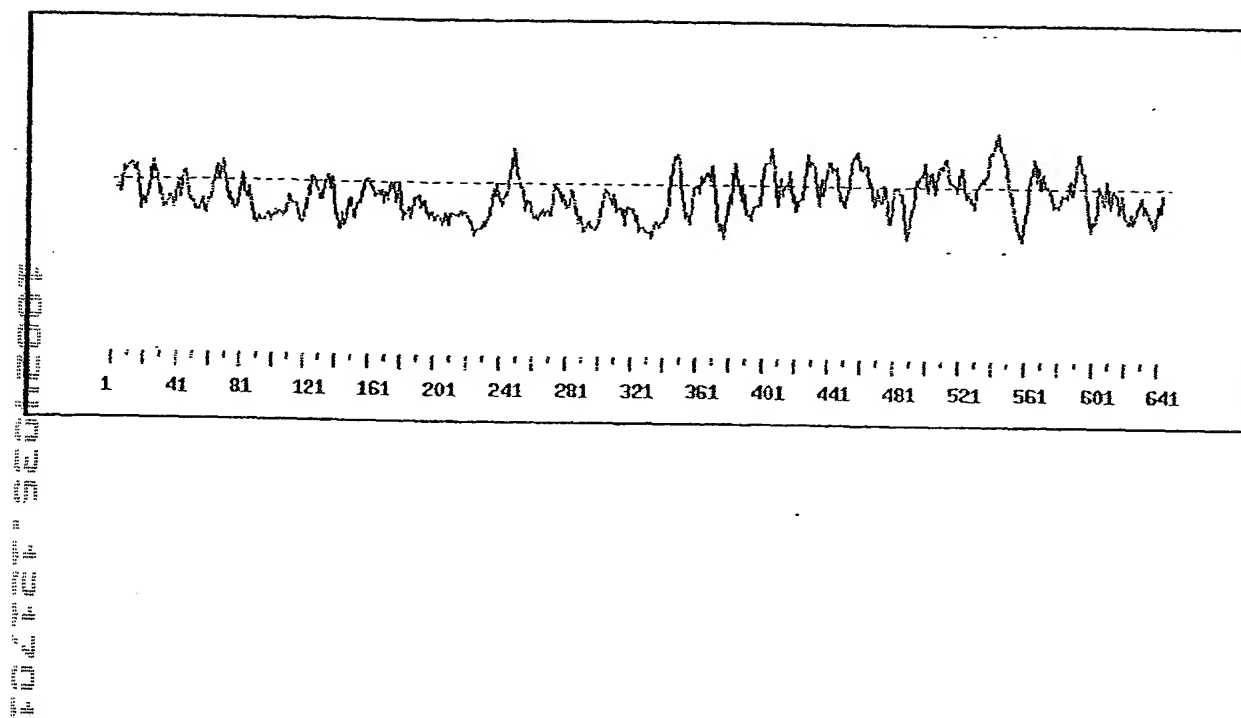


FIGURE 2

pkinase: domain 1 of 1, from 23 to 279: score 346.3, E = 3.4e-100
 *->yelleklGeGsfgGkVykakhk.tgkivAvKilkkels.....lrE
 +e++e+lG G+f++V +a++k tgk++AvK+++k+ l+++++ +E
 68730 23 FEFKETLGTGAFSEVVLAEKaTGKLFVVKCIPKKALKgkessiENE 69
 iqilkrIsHpNIvrlIlgvfedtddhlylvmEymegGdLfdyIrrngplse
 i++l++++H+NIV l +++e +++hlylvm+++ gG+Lfd++++g ++e
 68730 70 IAVLRKIKHENIVALEDIYE-SPNHLYLVMQLVSGGELFDRIVEKGFYTE 118
 keakkialQilrGleYlHsngivHRDLKpeNILlden...gtvKiaDFGL
 k+a +++Q+l ++ YLH++givHRDLKpeN+L +++++ ++ i+DFGL
 68730 119 KDAStLIROVLDAVYYLHRMGIVHRDLKPENLLYYSQdeeSKIMISDFGL 168
 Arll...eklttftvGTpwYmmAPEvilegrgysskvDvWSlGviLyEllt
 ++ +++ +ttt +GTp+Y+ APEv l +++ys++vD WS+Gvi y ll+
 68730 169 SKMEgkgDVMSTACGTPGYV-APEV-LAQKPYSKAVDCWSIGVIAIILLC 216
 ggplfpgadlpaftggdevdqliifvlklPfsdelpktridpleelfrik
 g +Pf+d ++ ++lf+ +
 68730 217 G-----YPPFYD-----ENDSKLFEQI 233
 kr.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<
 ++ + + +p ++ +S+++kd+++ + +kDP+kR+ t++++ hpw+
 68730 234 LKaeyefDSPYWDDISDSAKDFIRNLMEKDPNKRY---TCEQAARHPWI 279
 - *

FIGURE 3A

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serkin_6: domain 1 of 1, from 23 to 279: score 386.6, E = 2.5e-112
*->YellkklGkGaFGkVylardkktgrlvAiKvik.....erilrE
  +e+ ++lG GaF++V la +k tg+l+A+K+i+++ +++++ +i++E
68730  23  FEFKETLGTGAPSEVVLAEKATGKLFVAVKCIPkalkgkeSSIENE 69
      ↑                               ↑
      ikiLkk.dHPNIVKLydvfed.dklylVmEyceGdlGdLfdllkkrgrrg
      i++L+k +H+NIV L d++e++++lylVm +++G G+Lfd+++++g
68730  70  IAVLRKiKHENIVALEDIYESpNHLyLVMLVSG--GELFDRIVEKGF-- 115
      ↑                               ↑
      lrkvlse.earfyfrQilsaLeYLHsqqIiHRDLKPeNiLLds.....hv
      ++E+++ +trQ+l+a+ YLH++gI+HRDLKPeN+L s+++++ +
68730 116  ---YTEKDASTLIROVLDAVYYLHRMGIVHRDLKPENLLYYsQdeesKI 161
      ↑       ↑       ↑       ↑       ↑
      KladFGLArql.....ttfvGTpeYmAPEvl...gYgkpavDiWSlGci
      +++DFGL++ +++++ +t +GTP Y+APEvl +++Y+k avD WS+G+i
68730 162 MISDFGLSKMEgkgdvmSTACGTPGYVAPEVLaqkPYSK-AVDCWSIGVI 210
      lyElltGkpPFp..qldlifkkig.....SpeakdLikkll
      y+ll+G+pPF+++++ +f++i++ + ++++++ S++akd+i++l+
68730 211 AYILLCGYPFFYdeNDSKLFEQILkaeyefdsywdiSDSAKDFIRNLM 260
      vkdPekRlta.eaLedeldikaHPff<-*
      +kdP+kR+t+++a + HP++
68730 261 EKDPNKRYTCeQAAR-----HPWI 279
  
```

FIGURE 3B

tyrkin_6: domain 1 of 1, from 23 to 279: score 35.7, E = 4e-14
 *->ltlgkklGeGaFGeVykgTlk...ieVAVKtLkeda...keeFlrE
 +++++LG GaF eV+++ k ++ AVK++ + a +++ + +E
 68730 23 PEFKETLGTGAFSEVVLAEKtqKLFVAVKCIPKKalkgkESSIENE 69
 akiMkklGgkHpNiVklLlGvcteeGrFmevePlmivmEymegGdLldyL
 + +++k+ kH+NiV+L + ++ l++vm +++gG L d++
 68730 70 IAVLRKI--KHENIVALEDIYESP-----NHLVLMQLVSGGELFDRI 110
 rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
 ++ + +d Q+ + YL++++vHRDL N L+ ++ +++
 68730 111 -VEKGFYTEKDASTLIROVLDAVYVLRMGIVHRDLKPENLLYYSQDees 159
 vvKIsDFGLsRdlyddDkkGesKdyYrkkggkggkttlPirWmAPESlkd
 + IsDFGLs+ + + d+ +++ g+ + APE+l
 68730 160 KIMISDFGLSKMEGKG-----DVMSTAC--GTPG-----YVAPEVLAQ 195
 gkFtskSDVWSFGVlLWEiftlGeqPYpgeiqqfmsneevleylkkGyRl
 + ++ + D WS GV + i+ G +P ++ +++ ++e++ k ++
 68730 196 KPYSKAVDCWSIGVIAIY-ILLCGYPPFYD-----ENDSKLFEQILKAEYE 239
 pkPendlpisS...vtCPdelydlMlqCwaedPedRptFsel..verl<
 ++ ++ + + d + +lM++ dP++R t ++ ++ +
 68730 240 FDSPY-----WddisDSAKDFIRNLMEK----DPNKRYTCEQAarHPWI 279

FIGURE 3C

pkinese: domain 1 of 1, from 356 to 613: score 350.2, E = 2.3e-101
*->yelleklGeGsfgKvykakhk.tgkivAvKilkkesls.....lrE
ye++++G G+f++V++++h++t + +A+Ki++k++l++++ +E
69112 356 YETGRVIGDGNFAVVKECRHReTRQAYAMKIIDKSRLKgkedmvDSE 402

iqilkrIsHpNIvrlIlgvfedtddhlylvmEymegGdLfdylrrngplse
i i ++lsHpNIv+l++v+e td ++yl++Ey+ gGdLfd + + +++e
69112 403 ILIIQSLSHPNIVKLHEVYE-TDMEIYLILEYVQGGDLFDAIESVKFPE 451

keakkialQilrGleYlHsngivHRDLKpenILlden....gtvKiaDFG
++a ++ +++++l ++H+++ivHRDLKpen+L+ +n++++ t+K+aDFG
69112 452 PDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNedksTTLKLADFG 501

LArll.eklIttfvGTpwYmmAPEvilegrgysskvDvWSlGviLyElltg
LA+ + + t++Gtp+Y+ APE+ l+ +gy+ +vD+W+ GviLy ll+g
69112 502 LAKHVvRPIFTVCGTPTYV-APEI-LSEKGYGLEVDMWAAGVILYILLCG 549

gplfpgadlpaftggdevdqliifvklPfsdelpktridpleelfrikk
+Pf+ ++ +elf+i++
69112 550 -----FPPFRS-----PERDQDELFNIIQ 568

r.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<-
++ + ++p ++n+S+++kdL++++L +DP+kr+ ta+++l+hpw+
69112 569 LghfefLPPYWDNISDAAKDLVSRLLVVDPKKRY---TAHQVLQHPWI 613

FIGURE 4A

serkin_6: domain 1 of 1, from 356 to 613: score 372.7, E = 3.8e-108
 *->Yellkkk1GkGaFGkVylardkktgrlvAiKvik.....erilrE
 Ye ++++G G F++V+ +r+++t + +A+K+i++++ ++++++ +E
 69112 356 YETGRVIGDGNFAVVKECRHRETRQAYAMKIIDksrlkgkeDMVDSE 402
 ikiLkk.dHPNIVkLydvfed.dklylVmEyceGdlGdLfdllkkrgrrg
 i i ++ HPNIVkL++v+e++ ++yl++Ey+ G GdLfd + + +
 69112 403 ILIIQSLSHPNIVKLHEVYETdMEIYLLILEYVQG--GDLFDAIESVK-- 448
 lrvlsE.earfyfrQilsaLeYLHsqgIiHRDLKPeNiLLds.....h
 ++E++a+ ++ +++aL ++H++ I+HRDLKPeN+L+ ++++++
 69112 449 ----FPEpDAALMIMDLCKALVHMHDKSI[↑]VHRDLK[↑]PENLLVQRnedkstT 494
 vKlaDFGLArql....ttfvGTpeYmAPEvl...gYgkpavDiWSlGcil
 +KlaDFGLA+++ ++ t++GTp Y+APE+l+++gYg +vD+W+ G+il
 69112 495 LKLADFGLAHVvrpiFTVCGTPTYVAPEILsekGYGL-EVDMWAAGVIL 543
 yElltGkpPFp....qldlifkkig.....SpeakdLikk1
 y+ll+G pPF++++++d++f++i ++ + ++++++ S+ akdL+++l
 69112 544 YILLCGFPPFRsperDQDELFNIIQlghfeflppywdniSDAAKDLSRL 593
 LvkdPekRlta.eaLedeldikaHPff<-*
 Lv+dP+kR+ta+++L+ HP++
 69112 594 LVVDPKKRYTAhQVLQ-----HPWI 613

FIGURE 4B

tyrkin_6: domain 1 of 1, from 356 to 613: score 50.0, E = 5.3e-15
 *->ltlgkklGeGaFGeVykGtlk...ieVAVKtLkeda....keeFlrE
 + g+++G G+F +V +++ +++++ A K + ++ +++++ + +E
 69112 356 YETGRVIGDGNFAVVKECRHRetrQAYAMKIIDKSRLkgkEDMVDSE 402
 akiMkklGgkHpNiVklLgVcteegrrFmevePlmivmEymegGdLldyL
 + i +l +HpNiVkl+ v ++ +++++Ey+ gGdL d +
 69112 403 ILIIQSL--SHPNIVKLHEVYETD-----MEIYLILEYVQGGDLFDAI 443
 rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
 ++ + ++ +d + + +k + ++k +vHRDL N Lv +n +++
 69112 444 IESVK-FPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEdks 492
 .vvKIsDFGLsRdlyddDkkGeskdYrkkggkggktilPirWmAPESlk
 ++ K +DFGL++ + ++ +g APE l
 69112 493 tTLKLADFLAKHVVRP-----IFTV----CGTP----TYVAPEILS 526
 dgkFtskSDVWSFGVlLWEiftlGeqPYpgeiqqfmsneevleylkkGyR
 ++ + + D W+ GV L+ i+ G +P ++ + +e+++ ++ G+
 69112 527 EKGYLEVDMWAAGVILY-ILLCGFPPFRSPE---RDQDELFNIIQLGHF 572
 lpkPendlpisSvtCPdelydlMlqCwaedPedRPtFsel..verl<-*
 P++ +d+ dl ++ dP++R t ++ ++ +
 69112 573 EFLPPY-----WDNISDAAKDLVSRLLVVDPKKRYTAHQVlqHPWI 613

FIGURE 4C